

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 25, 2001, 09:26:12 ; Search time 22.69 Seconds

Title: US-09-829-931-2
Perfect score: 1298
Sequence: 1 MKNNWTRLFKVLLGPFRLR DVKNALEGKGYPEGTAPSQ 245

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

20 161 12.4 243 2 09zD75
21 160.5 12.4 295 2 054097
22 160.5 12.4 626 2 09kqn2
23 159.5 12.3 223 2 09kqr1
24 153.5 11.8 408 10 09ma64
25 153 11.8 242 2 09k3r3
26 148.5 11.4 213 2 09ra7
27 148 11.4 212 2 09z7y4
28 147 11.3 251 2 007808
29 146 11.2 199 2 007584
30 142 10.9 261 2 007809
31 131 10.1 1170 2 09pnz5
32 130.5 10.1 240 2 P73054
33 129 9.9 275 2 006830
34 121.5 9.4 287 2 053962
35 119.5 9.2 253 2 09p1e8
36 117.5 9.1 253 2 09js89
37 116.5 9.0 253 2 0926y5
38 116 8.9 252 2 09wlk9
39 116 8.9 271 5 09xzt8
40 115.5 8.9 237 2 09zjn8
41 115 8.9 252 2 094f82
42 114.5 8.8 352 5 09var3
43 113 8.7 253 2 084180
44 111.5 8.6 279 2 09vz05
45 109.5 8.4 247 2 09jxt4

ALIGNMENTS

RESULT 1
ID Q9KKE6 PRELIMINARY;
AC Q9KKE6;

DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)

DE HYPOTHETICAL 27.1 KDA PROTEIN.

OS Corynebacterium glutamicum (Brevibacterium flavidum).
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Corynebacteriaceae;
OC Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC13032;
RA Lee, J.-K., Park, S.Y.;

RT "The glucose kinase gene of Corynebacterium glutamicum."
RL Submitted (Oct-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF096280; AAF80162.1; -.
KW Hypothetical Protein
SQ SEQUENCE 245 AA; 2714 MW; 6E87F521A8134878 CRC64;

Query No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query	Match Length	DB ID	Description
1	1298	100.0	245	2 Q9KKE6	Q9kke6 corynebacteri
2	575	44.3	244	2 069572	069572 mycobacteri
3	566	43.6	247	2 053516	053516 mycobacteri
4	499	38.4	262	2 Q9SM2	Q9sm2 streptomyce
5	478	36.8	223	2 Q9LB5	Q9lb5 streptomyce
6	413	31.8	199	2 033970	033970 streptomyce
7	252	19.5	211	2 067841	067841 aquifex aeo
8	246.5	19.0	247	2 09X219	09x219 thermotoga
9	226	17.4	823	2 067119	067119 aquifex aeo
10	223	17.2	216	2 Q9P0T9	Q9p0t9 chlamydia m
11	217.5	16.8	264	2 Q9ZBS1	Q9zbs1 streptomyce
12	215.5	16.6	195	2 Q9KCD7	Q9kcd7 bacillus ha
13	212.5	16.4	225	2 P74498	P74498 synechocyst
14	212	16.3	216	2 084459	084459 chlamydia t
15	202	15.6	212	10 Q9M0A2	Q9m0a2 arabidopsis
16	181	13.9	344	10 Q9LJY4	Q9ljy4 brassica na
17	173.5	13.4	259	2 007807	007807 mycobacteri
18	171.5	13.2	355	2 Q9NWX9	Q9nx9 streptomyce
19	169.5	13.1	281	10 Q9SDQ2	Q9sdq2 limnanthes

Query Match 100.0%; Score 1298; DB 2; Length 245;
Best Local Similarity 100.0%; Pred. No. 1e-108; Mismatches 0; Indels 0; Gaps 0;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MKNNWTRLFKVLLGPFRLR DVKNALEGKGYPEGTAPSQ 245
1 MKNNWTRLFKVLLGPFRLR DVKNALEGKGYPEGTAPSQ 245
1 PEGSRSPDRYIKGKGTGMAYAMETGTIVIPAMIGSRDANP1GSWPKPAVKYKGS 180
1 MKNNWTRLFKVLLGPFRLR DVKNALEGKGYPEGTAPSQ 245
1 IDPLAFYKEHGLKP GTYEAARKLTDHYMFILADLTGQPYDAYS KDVYNALEFGK YPEG 240

